

SEQUENCE LISTING

<110> MCGILL UNIVERSITY
SZYF, Moshe
BHATTACHARYA, Sanjoy K.
RAMCHANDANI, Shyam

<120> DNA DEMETHYLASE, THERAPEUTIC AND
DIAGNOSTIC USES THEREOF

<130> 1770-183 "PCT" FC/ld

<150> CA 2,220,805

<151> 1997-11-12

<150> CA 2,230,991

<151> 1998-05-11

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1804

<212> DNA

<213> Unknown

<400> 1

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agcagggg	ccagggc	gcgctc	cgtccccg	gagcggcg	cgcaggga	240
gcgctcgg	cggcgccg	ggccgggg	ggtggaag	ggcggccc	ggcggcgg	300
tctgtggc	tggccgtg	cgtggccg	gtcggggc	tgccgggg	cggggccg	360
gccgcggc	tccccag	ggcggc	gccttg	cgacggcg	ggcggc	420
gcggctgc	cgtcggc	ggtggc	tgcggggc	gcgggatc	gtcccttc	480
cgtcgggg	ctcggggc	gggccc	gacccggg	cacggag	gggaagag	540
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tcagtgtc	caagagc	gtctact	tcagtc	tggtaga	ttcaga	660
aacctcag	ggcaagat	ctgggaa	ctgtgac	tagcagtt	gacttcag	720
ccggcaag	gatgcct	aaattac	agaaca	gagactcc	aatgaccc	780
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caattttc	gcaacc	accaa	cgaacc	gagcaat	gtgaagtc	900
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aacaga	aat	actg	gcctg	aaaag	ctgag	1440
agcttt	ta	caatg	ttag	tttg	tata	1500
attcc	aat	atg	tga	gact	taag	1560
caggg	cc	cggt	gcag	ggcc	agtg	1620
cttac	gt	gaa	atatt	gt	tt	1680

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 <211> 411
 <212> PRT
 <213> Unknown

<400> 2

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 35 40 45
 Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
 50 55 60
 Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
 65 70 75 80
 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
 85 90 95
 Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
 100 105 110
 Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
 115 120 125
 Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
 130 135 140
 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
 145 150 155 160
 Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
 165 170 175
 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
 180 185 190
 Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
 195 200 205
 Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
 210 215 220
 Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
 225 230 235 240
 Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 245 250 255
 Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 260 265 270
 Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
 275 280 285
 Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
 290 295 300
 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
 305 310 315 320
 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
 325 330 335
 Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
 340 345 350
 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
 355 360 365

009060-1115560

Sub B

Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
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 Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
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 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
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 <212> DNA
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 cttcaataaa ctgatggtag gaacttgtg 1589

<210> 4
 <211> 291
 <212> PRT
 <213> Unknown

<400> 4

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 35 40 45
 Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
 50 55 60
 Arg Thr Gly Lys Met Leu Met Ser Lys Met Asn Lys Ser Arg Gln Arg
 65 70 75 80

Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
 85 90 95
 Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 100 105 110
 Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 115 120 125
 Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
 130 135 140
 Gly Leu Asn Ala Phe Asp Ile Ala Glu Glu Leu Val Lys Thr Met Asp
 145 150 155 160
 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
 165 170 175
 Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Met Pro Ile
 180 185 190
 Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
 195 200 205
 Asn Thr Thr Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Glu Asp
 210 215 220
 Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
 225 230 235 240
 Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
 245 250 255
 Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Asp Asp Glu
 260 265 270
 Glu Asp Glu Glu Glu Glu Glu Glu Pro Asp Pro Asp Pro Glu Met
 275 280 285
 Glu His Val
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<210> 5
 <211> 1966
 <212> DNA
 <213> Unknown

<400> 5

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cggcgctggc	ggcgactccg	ccatagagca	ggggggccag	ggcagcgcg	tcgccccgtc	360
cccgtgagc	ggcgtgcgca	gggaaggcgc	tcggggcggc	ggccgtggcc	gggggcgggtg	420
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 <212> PRT
 <213> Unknown

<400> 6

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 35 40 45
 Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
 50 55 60
 Lys Gln Ala Ala Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
 65 70 75 80
 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
 85 90 95
 Pro Gln Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Ala
 100 105 110
 Gly Gly Cys Gly Val Gly Ser Gly Gly Val Ala Pro Arg Arg Asp
 115 120 125
 Pro Val Pro Phe Pro Ser Gly Ser Ser Gly Pro Gly Pro Arg Gly Pro
 130 135 140
 Arg Ala Thr Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro
 145 150 155 160
 Gly Trp Lys Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly
 165 170 175
 Lys Ser Asp Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser
 180 185 190
 Lys Pro Gln Leu Ala Arg Tyr Leu Gly Asn Ala Val Asp Leu Ser Ser
 195 200 205
 Phe Asp Phe Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn
 210 215 220
 Lys Gln Arg Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro
 225 230 235 240
 Asp Leu Asn Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys
 245 250 255
 Gln Pro Val Thr Lys Phe Thr Asn His Pro Ser Asn Lys Val Lys Ser
 260 265 270
 Asp Pro Gln Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys
 275 280 285
 Arg Leu Gln Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys
 290 295 300

009060-11113360

Sub B1

Thr Met Glu Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn
 305 310 315 320
 Asp Glu Thr Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser
 325 330 335
 Ala Pro Ile Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala
 340 345 350
 Val Trp Leu Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr
 355 360 365
 Asp Glu Asp Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys
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 Lys Leu Glu Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp
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 Thr Glu Glu Val Asp Ile Asp Met Asp Ser Gly Asp Glu Ala
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 <211> 2392
 <212> DNA
 <213> Unknown

<400> 7

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 <213> Unknown

<400> 8

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 35 40 45
 Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
 50 55 60
 Arg Thr Gly Lys Met Leu Met Asn Lys Met Asn Lys Ser Arg Gln Arg
 65 70 75 80
 Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
 85 90 95
 Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 100 105 110
 Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 115 120 125
 Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
 130 135 140
 Gly Leu Ser Ala Phe Asp Ile Ala Glu Glu Leu Val Arg Thr Met Asp
 145 150 155 160
 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
 165 170 175
 Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Leu Pro Ile
 180 185 190
 Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
 195 200 205
 Asn Thr Ala Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Asp Asp
 210 215 220
 Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
 225 230 235 240
 Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
 245 250 255
 Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Glu Glu Glu Glu
 260 265 270
 Glu Glu Glu Glu Glu Glu Glu Pro Glu Pro Glu Arg Val
 275 280 285

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 <212> DNA
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<400> 9

ctggcaagag cgatgtc

~~<210> 10~~
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22

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